REMARKS/ARGUMENTS

Status of the Claims

Upon entry of the above amendment, Claims 1-11 and 40-42 are pending. Claims 1-2, 4-5, 7 and 8 are amended. Claims 40-42 are newly added

Claim 1 is amended to recite "at least 70% amino acid sequence identity." Claim 2 is amended to recite that the protein is "at least 80% identical." New Claims 40 and 41 recite that the protein is at least 90 and 95% identical, respectively. Support is found, for example, on page 10, lines 11-14, page 11, lines 19-25, page 18, lines 18-25 and page 45, lines 20-21.

Claim 4 is amended to recite a nucleotide sequence "at least 80% identical." Claims 5 is amended to recite a nucleotide sequence "at least 90% identical." New Claim 42 recites that the nucleotide sequence is at least 95% identical. Support is found, for example, on page 18, lines 18-25.

Claims 7 and 8 are amended to recite specific hybridization conditions. Support is found, for example, on page 22, lines 14-17 and 22-24.

Amendments to the Specification

Support for spelling out the acronyms "ERα" and "ERβ" on page 2, line 17 is found, for example, on page 1, lines 19 and 25.

Support for spelling out the acronym "SH3" on page 2, line 7 is found, for example, on page 12, line 23.

Support for spelling out the acronym "RT-PCR" on page 6, line 24 is found, for example, on page 47, lines 1-2.

Objections to the Specification

The Examiner has requested that the terms "ERα," "ERβ," "SH3," "RT-PCR" and "RACE" be spelled out in their first instance of use in the specification. In accordance with the Examiner's suggestion, Applicants have amended the relevant paragraphs to recite the full spelling of the acronyms "ERα," "ERβ," "SH3" and "RT-PCR" in their first instance.

Applicants have not spelled out the acronym for "RACE," because it is well known to those in the art to mean "rapid amplification of cDNA ends," a particular polymerase chain reaction (PCR) technique. For instance, since January 1990 until the March 2001 filing date of the instant application, "RACE" was defined as "rapid amplification of cDNA ends" in at least 443 scientific publications.[1]

Rejection under 35 U.S.C. § 112, Written Description Requirement

The Examiner has rejected Claims 1-11 under 35 U.S.C. § 112, first paragraph, because the specification allegedly does not show possession of the genus of polypeptides and polynucleotides recited in the originally filed claims. In this rejection, the Examiner has conflated the standards set forth for written description and enablement. For the purposes of responding, Applicants assume that the Examiner intended this to be a written description rejection, because the Examiner directs Applicants to the written description guidelines on pages 4 and 5 of paper 11.

As amended, Claim 1 recites an isolated nucleic acid encoding a protein comprising at least 70% amino acid identity to SEQ ID NO:1, SEQ ID NO:4 or SEQ ID NO:6. Amended Claim 4 recites that the isolated nucleic acid comprises a nucleotide sequence that is at least 80% identical to SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7. All claims ultimately depend from Claim 1.

Applicants respectfully traverse this rejection because the specification objectively demonstrates possession of an isolated nucleic acid encoding an estrogen-regulated unconventional myosin-related protein (MRP) comprising at least 70% sequence identity to SEQ ID NO:1, SEQ ID NO:4 or SEQ ID NO:6 as currently claimed. Applicants demonstrate possession of at least four MRP nucleic acid variants, two from mouse and two from human, as depicted by SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7, and at least three MRP polypeptide variants, as depicted by SEQ ID NO:1, SEQ ID NO:4 and SEQ ID NO:6 in the

[1] The first page of a search for "rapid amplification of cdna ends AND RACE" with date limits of 01/01/1990 through 03/09/2001 in the PubMed database (www.ncbi.nlm.nih.gov/entrez) is attached as Exhibit A.

sequence listing on pages 63-75 of the specification. Executing BLAST2 alignments of the nucleic acid and amino acid sequences using the algorithms (blastn and blastp) provided through the National Center for Biotechnological Information demonstrates that the interspecies homolog variants (i.e., comparison of the mouse and human sequences) share 66% and 69% amino acid identity and 81% nucleic acid identity.[2] Figure 8 shows that aligned human and mouse MRP amino acid sequences share 74% sequence identity. Therefore, Applicants are objectively in possession of an isolated nucleic acid encoding an estrogen-regulated unconventional myosin-related protein comprising at least 70% identity to SEQ ID NO:1, SEQ ID NO:4 or SEQ ID NO:6, as recited in Claim 1. Further, Applicants are also objectively in possession of an isolated nucleic acid encoding an estrogen-regulated unconventional myosin-related protein, wherein the nucleic acid is at least 80% identical to SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7, as recited in Claim 4. Because Applicants claim an isolated nucleic acid encoding an estrogen-regulated unconventional myosin-related protein, the claimed nucleic acids are structurally and functionally related.

Additionally, the specification explicitly teaches on page 10, lines 11-14 that amino acid identity of at least 70-95% typically demonstrates that a protein is a polymorphic variant, interspecies homolog, or allele of the MRP protein. On page 11, lines 21-24, the specification teaches that the term MRP refers to polymorphic variants, alleles, mutants and interspecies homologs that have about 60-95% amino acid identity to SEQ ID NO:1, SEQ ID NO:4 or SEQ ID NO:6. The specification teaches on page 18, lines 18-22 that the terms "identical" or "percent identity" in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that have a specified percentage of amino acid residues or nucleotides that are the same (i.e., 70-95%). In the section teaching "Assays for MRP Protein Activity" beginning on page 45, the specification teaches using MRP protein variants having at least 70-95% amino acid sequence identity (page 45, lines 16-21).

[2] www.ncbi.nlm.nih.gov/blast/bl2seq. The first pages of all Blast2 sequence alignment results using default settings are attached as Exhibit B.

For the foregoing reasons, the Examiner is respectfully requested to withdraw this rejection.

Rejection under 35 U.S.C. § 112, Second Paragraph

The Examiner has rejected Claims 1 and 4 for reciting "at least about ..." This rejection is obviated by amending Claims 1 and 4 to recite "at least ..."

Claims 1 and 4 were further rejected for reciting sequence similarity. This rejection is obviated by amending Claims 1 and 4 to recite "sequence identity."

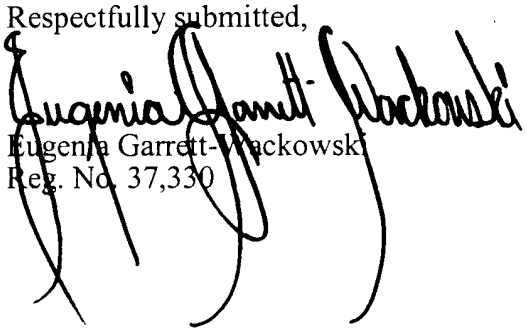
Claims 7 and 8 were rejected for not reciting specific hybridization and wash conditions. This rejection is obviated by amending Claims 7 and 8 to recite specific hybridization and wash conditions, as suggested by the Examiner.

CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 925-472-5000.

Respectfully submitted,



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